RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/525,019_

Source: _Pu7/10_

Date Processed by STIC: _9/1/05_

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RAW SEQUENCE LISTING   DATE: 09/01/2005
PATENT APPLICATION: US/10/525,019   TIME: 15:47:04

Input Set : A:\GIES3002.ST25.txt
Output Set: N:\CRF4\09012005\J525019.raw

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 3 <110> APPLICANT: Giesing, Michael
 4       Suchy, Bernhard
 6 <120> TITLE OF INVENTION: METHOD FOR ANALYZING BODY FLUIDS FOR THE PRESENCE OF CANCER
 7       CELLS, USE THEREOF, CORRESPONDING ANALYSIS KITS, AND USE OF
 8       SPECIFIC ACTIVE SUBSTANCES FOR TREATING CANCER
10 <130> FILE REFERENCE: GIES3002
12 <140> CURRENT APPLICATION NUMBER: 10/525,019
13 <141> CURRENT FILING DATE: 2005-02-18
15 <150> PRIOR APPLICATION NUMBER: PCT/EP03/009229
16 <151> PRIOR FILING DATE: 2003-08-20
18 <150> PRIOR APPLICATION NUMBER: DE 102 38 046.5
19 <151> PRIOR FILING DATE: 2002-08-20
21 <160> NUMBER OF SEQ ID NOS: 22
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 22
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial
30 <220> FEATURE:
31 <223> OTHER INFORMATION: forward primer (MNSOD)
33 <400> SEQUENCE: 1
34 gtcaccgagg agaagtacca gg                              22
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 20
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial
42 <220> FEATURE:
43 <223> OTHER INFORMATION: reverse primer (MNSOD)
45 <400> SEQUENCE: 2
46 gggctgaggt ttgtccagaa                                 20
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 27
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial
54 <220> FEATURE:
55 <223> OTHER INFORMATION: probe (MNSOD)
57 <400> SEQUENCE: 3
58 cgttggccaa gggagatgtt acagccc                         27
61 <210> SEQ ID NO: 4
62 <211> LENGTH: 23
63 <212> TYPE: DNA
64 <213> ORGANISM: Artificial
66 <220> FEATURE:
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67 <223> OTHER INFORMATION: forward primer (TXNRD1)
69 <400> SEQUENCE: 4
70 ggagggcaga cttcaaaagc tac                                    23
73 <210> SEQ ID NO: 5
74 <211> LENGTH: 22
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial
78 <220> FEATURE:
79 <223> OTHER INFORMATION: reverse primer (TXNRD1)
81 <400> SEQUENCE: 5
82 acaaagtcca ggaccatcac ct                                     22
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 26
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial
90 <220> FEATURE:
91 <223> OTHER INFORMATION: probe (TXNRD1)
93 <400> SEQUENCE: 6
94 ttgggctgcc tccttagcag ctgcca                                 26
97 <210> SEQ ID NO: 7
98 <211> LENGTH: 17
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial
102 <220> FEATURE:
103 <223> OTHER INFORMATION: forward primer (GPX1)
105 <400> SEQUENCE: 7
106 ctcggcttcc cgtgcaa                                           17
109 <210> SEQ ID NO: 8
110 <211> LENGTH: 19
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial
114 <220> FEATURE:
115 <223> OTHER INFORMATION: reverse primer (GPX1)
117 <400> SEQUENCE: 8
118 tgaagttggg ctcgaaccc                                         19
121 <210> SEQ ID NO: 9
122 <211> LENGTH: 28
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial
126 <220> FEATURE:
127 <223> OTHER INFORMATION: probe (GPX1)
129 <400> SEQUENCE: 9
130 agtttgggca tcaggagaac gccaagaa                               28
133 <210> SEQ ID NO: 10
134 <211> LENGTH: 19
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial
138 <220> FEATURE:
139 <223> OTHER INFORMATION: forward primer (GAPDH)
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142 tgctgatgcc cccatgttc                                           19
145 <210> SEQ ID NO: 11
146 <211> LENGTH: 20
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial
150 <220> FEATURE:
151 <223> OTHER INFORMATION: reverse primer (GAPDH)
153 <400> SEQUENCE: 11
154 ggcagtgatg gcatggactg                                          20
157 <210> SEQ ID NO: 12
158 <211> LENGTH: 27
159 <212> TYPE: DNA
160 <213> ORGANISM: Artificial
162 <220> FEATURE:
163 <223> OTHER INFORMATION: probe (GAPDH)
165 <400> SEQUENCE: 12
166 tcaagatcat cagcaatgcc tcctgca                                  27
169 <210> SEQ ID NO: 13
170 <211> LENGTH: 222
171 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 13
176 Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala
177 1               5                   10                  15
180 Leu Gly Tyr Leu Gly Ser Arg Gln Lys His Ser Leu Pro Asp Leu Pro
181             20                  25                  30
184 Tyr Asp Tyr Gly Ala Leu Glu Pro His Ile Asn Ala Gln Ile Met Gln
185         35                  40                  45
188 Leu His His Ser Lys His His Ala Ala Tyr Val Asn Asn Leu Asn Val
189     50                  55                  60
192 Thr Glu Glu Lys Tyr Gln Glu Ala Leu Ala Lys Gly Asp Val Thr Ala
193 65                  70                  75                  80
196 Gln Thr Ala Leu Gln Pro Ala Leu Lys Phe Asn Gly Gly Gly His Ile
197                 85                  90                  95
200 Asn His Ser Ile Phe Trp Thr Asn Leu Ser Pro Asn Gly Gly Gly Glu
201             100                 105                 110
204 Pro Lys Gly Glu Leu Leu Glu Ala Ile Lys Arg Asp Phe Gly Ser Phe
205         115                 120                 125
208 Asp Lys Phe Lys Glu Lys Leu Thr Ala Ala Ser Val Gly Val Gln Gly
209         130                 135                 140
212 Ser Gly Trp Gly Trp Leu Gly Phe Asn Lys Glu Arg Gly His Leu Gln
213 145                 150                 155                 160
216 Ile Ala Ala Cys Pro Asn Gln Asp Pro Leu Gln Gly Thr Thr Gly Leu
217             165                 170                 175
220 Ile Pro Leu Leu Gly Ile Asp Val Trp Glu His Ala Tyr Tyr Leu Gln
221         180                 185                 190
224 Tyr Lys Asn Val Arg Pro Asp Tyr Leu Lys Ala Ile Trp Asn Val Ile
225         195                 200                 205
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228 Asn Trp Glu Asn Val Thr Glu Arg Tyr Met Ala Cys Lys Lys
229     210                 215             220
232 <210> SEQ ID NO: 14
233 <211> LENGTH: 976
234 <212> TYPE: DNA
235 <213> ORGANISM: Homo sapiens
237 <400> SEQUENCE: 14
238 gcgggcggcg caggagcggc actcgtggct gtggtggctt cggcagcggc ttcagcagat   60
240 cggcggcatc agcggtagca ccagcactag cagcatgttg agccgggcag tgtgcggcac  120
242 cagcaggcag ctggctccgg ctttggggta tctgggctcc aggcagaagc acagcctccc  180
244 cgacctgccc tacgactacg gcgccctgga acctcacatc aacgcgcaga tcatgcagct  240
246 gcaccacagc aagcaccacg cggcctacgt gaacaacctg aacgtcaccg aggagaagta  300
248 ccaggaggcg ttggccaagg gagatgttac agcccagaca gctcttcagc ctgcactgaa  360
250 gttcaatggt ggtggtcata tcaatcatag cattttctgg acaaacctca gccctaacgg  420
252 tggtggagaa cccaaagggg agttgctgga agccatcaaa cgtgactttg gttcctttga  480
254 caagtttaag gagaagctga cggctgcatc tgttggtgtc caaggctcag gttggggttg  540
256 gcttggtttc aataaggaac ggggacactt acaaattgct gcttgtccaa atcaggatcc  600
258 actgcaagga acaacaggcc ttattccact gctggggatt gatgtgtggg agcacgctta  660
260 ctaccttcag tataaaaatg tcaggcctga ttatctaaaa gctatttgga atgtaatcaa  720
262 ctgggagaat gtaactgaaa gatacatggc ttgcaaaaag taaaccacga tcgttatgct  780
264 gagtatgtta agctctttat gactgttttt gtagtggtat agagtactgc agaatacagt  840
266 aagctgctct attgtagcat ttcttgatgt tgcttagtca cttatttcat aaacaactta  900
268 atgttctgaa taatttctta ctaaacattt tgttattggg caagtgattg aaaatagtaa  960
270 atgctttgtg tgattg                                                   976
273 <210> SEQ ID NO: 15
274 <211> LENGTH: 497
275 <212> TYPE: PRT
276 <213> ORGANISM: Homo sapiens
278 <400> SEQUENCE: 15
280 Met Asn Gly Pro Glu Asp Leu Pro Lys Ser Tyr Asp Tyr Asp Leu Ile
281 1               5                   10                  15
284 Ile Ile Gly Gly Gly Ser Gly Gly Leu Ala Ala Ala Lys Glu Ala Ala
285             20                  25                  30
288 Gln Tyr Gly Lys Lys Val Met Val Leu Asp Phe Val Thr Pro Thr Pro
289         35                  40                  45
292 Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys
293     50                  55                  60
296 Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gln Ala Leu
297 65                  70                  75                  80
300 Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu Glu Thr Val Lys His
301                 85                  90                  95
304 Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn His Ile Gly Ser Leu
305             100                 105                 110
308 Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys Lys Val Val Tyr Glu
309         115                 120                 125
312 Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg Ile Lys Ala Thr Asn
313     130                 135                 140
316 Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu Ser Phe Leu Ile Ala
317 145                 150                 155                 160
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320 Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro Gly Asp Lys Glu Tyr
321             165             170             175
324 Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro Tyr Cys Pro Gly Lys
325         180             185             190
328 Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe
329         195             200             205
332 Leu Ala Gly Ile Gly Leu Gly Val Thr Val Met Val Arg Ser Ile Leu
333     210             215             220
336 Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys Ile Gly Glu His Met
337 225             230             235             240
340 Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val Pro Ile Lys Val
341             245             250             255
344 Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu Arg Val Val Ala Gln
345         260             265             270
348 Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu Tyr Asn Thr Val Met
349         275             280             285
352 Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys Ile Gly Leu Glu Thr
353     290             295             300
356 Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys Ile Pro Val Thr Asp
357 305             310             315             320
360 Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala Ile Gly Asp Ile Leu
361             325             330             335
364 Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile Gln Ala Gly Arg Leu
365         340             345             350
368 Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val Lys Cys Asp Tyr Glu
369         355             360             365
372 Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Ala Cys Gly
373     370                 375             380
376 Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly Glu Glu Asn Ile Glu
377 385             390             395             400
380 Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp Thr Ile Pro Ser Arg
381             405             410             415
384 Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys Asn Thr Lys Asp Asn
385         420             425             430
388 Glu Arg Val Val Gly Phe His Val Leu Gly Pro Asn Ala Gly Glu Val
389         435             440             445
392 Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly Leu Thr Lys Lys Gln
393     450             455             460
396 Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys Ala Glu Val Phe Thr
397 465             470             475             480
400 Thr Leu Ser Val Thr Lys Arg Ser Gly Ala Ser Ile Leu Gln Ala Gly
401             485             490             495
404 Cys
408 <210> SEQ ID NO: 16
409 <211> LENGTH: 1314
410 <212> TYPE: DNA
411 <213> ORGANISM: Homo sapiens
413 <400> SEQUENCE: 16
414 gaattcgggt ggagtcctga aggagggcct gatgtcttca tcattctcaa attcttgtaa        60
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<u>Invalid <213> Response:</u>
**Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.**

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,19,20,21,22

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